

RAW SEQUENCE LISTING

DATE: 01/04/2002

PATENT APPLICATION: US/09/921,922A

TIME: 15:05:42

Input Set : A:\16516-107 seq listing.txt

Output Set: N:\CRF3\01042002\I921922A.raw

1 <110> APPLICANT: Boronat, Albert;
2 Campos, Narciso;
3 Rodriguez-Concepcion, Manuel;
4 Rohmer, Michel;
5 Seeman, Myriam;
6 Valentin, Henry E.;
7 Venkatesh, Tyamagondlu V.;
8 Venkatramesh, Mylavarapu
10 <120> TITLE OF INVENTION: Methyl-D-Erythritol Phosphate Pathway Genes
12 <130> FILE REFERENCE: 16516.107/35-21(51897)US
14 <140> CURRENT APPLICATION NUMBER: US/09/921,922A
14 <141> CURRENT FILING DATE: 2001-12-19
14 <150> PRIOR APPLICATION NUMBER: US 60/223,483
15 <151> PRIOR FILING DATE: 2000-08-07
17 <160> NUMBER OF SEQ ID NOS: 85
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21 <212> TYPE: DNA
22 <213> ORGANISM: Arabidopsis thaliana
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (154)..(2376)
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34 ctcgtcttca gttactttga ttactgaga aaa atg gcg act gga gta ttg cca 174
35 Met Ala Thr Gly Val Leu Pro
36 1 5
38 gct ccg gtt tct ggg atc aag ata ccg gat tcg aaa gtc ggg ttt ggt 222
39 Ala Pro Val Ser Gly Ile Lys Ile Pro Asp Ser Lys Val Gly Phe Gly
40 10 15 20
42 aaa agc atg aat ctt gtg aga att tgt gat gtt agg agt cta aga tct 270
43 Lys Ser Met Asn Leu Val Arg Ile Cys Asp Val Arg Ser Leu Arg Ser
44 25 30 35
46 gct agg aga aga gtt tcg gtt atc cgg aat tca aac caa ggc tct gat 318
47 Ala Arg Arg Arg Val Ser Val Ile Arg Asn Ser Asn Gln Gly Ser Asp
48 40 45 50 55
50 tta gct gag ctt caa cct gca tcc gaa gga agc cct ctc tta gtg cca 366
51 Leu Ala Glu Leu Gln Pro Ala Ser Glu Gly Ser Pro Leu Leu Val Pro
52 60 65 70
54 aga cag aaa tat tgt gaa tca ttg cat aag acg gtg aga agg aag act 414
55 Arg Gln Lys Tyr Cys Glu Ser Leu His Lys Thr Val Arg Arg Lys Thr
56 75 80 85
58 cgt act gtt atg gtt gga aat gtc gcc ctt gga agc gaa cat ccg ata 462
59 Arg Thr Val Met Val Gly Asn Val Ala Leu Gly Ser Glu His Pro Ile
60 90 95 100
62 agg att caa acg atg act act tcg gat aca aaa gat att act gga act 510

ENTERED

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66 gtt gat gag gtt atg aga ata gcg gat aaa gga gct gat att gta agg 558
67 Val Asp Glu Val Met Arg Ile Ala Asp Lys Gly Ala Asp Ile Val Arg
68 120 125 130 135
70 ata act gtt caa ggg aag aaa gag gcg gat gcg tgc ttt gaa ata aaa 606
71 Ile Thr Val Gln Gly Lys Lys Glu Ala Asp Ala Cys Phe Glu Ile Lys
72 140 145 150
74 gat aaa ctc gtt cag ctt aat tac aat ata ccg ctg gtt gca gat att 654
75 Asp Lys Leu Val Gln Leu Asn Tyr Asn Ile Pro Leu Val Ala Asp Ile
76 155 160 165
78 cat ttt gcc cct act gta gcc tta cga gtc gct gaa tgc ttt gac aag 702
79 His Phe Ala Pro Thr Val Ala Leu Arg Val Ala Glu Cys Phe Asp Lys
80 170 175 180
82 atc cgt gtc aac cca gga aat ttt gcg gac agg cgg gcc cag ttt gag 750
83 Ile Arg Val Asn Pro Gly Asn Phe Ala Asp Arg Arg Ala Gln Phe Glu
84 185 190 195
86 acg ata gat tat aca gaa gat gaa tat cag aaa gaa ctc cag cat atc 798
87 Thr Ile Asp Tyr Thr Glu Asp Glu Tyr Gln Lys Glu Leu Gln His Ile
88 200 205 210 215
90 gag cag gtc ttc act cct ttg gtt gag aaa tgc aaa aag tac ggg aga 846
91 Glu Gln Val Phe Thr Pro Leu Val Glu Lys Cys Lys Lys Tyr Gly Arg
92 220 225 230
94 gca atg cgt att ggg aca aat cat gga agt ctt tct gac cgt atc atg 894
95 Ala Met Arg Ile Gly Thr Asn His Gly Ser Leu Ser Asp Arg Ile Met
96 235 240 245
98 agc tat tac ggg gat tct ccc cga gga atg gtt gaa tct gcg ttt gag 942
99 Ser Tyr Tyr Gly Asp Ser Pro Arg Gly Met Val Glu Ser Ala Phe Glu
100 250 255 260
102 ttt gca aga ata tgt cgg aaa tta gac tat cac aac ttt gtt ttc tca 990
103 Phe Ala Arg Ile Cys Arg Lys Leu Asp Tyr His Asn Phe Val Phe Ser
104 265 270 275
106 atg aaa gcg agc aac cca gtg atc atg gtc cag gcg tac cgt tta ctt 1038
107 Met Lys Ala Ser Asn Pro Val Ile Met Val Gln Ala Tyr Arg Leu Leu
108 280 285 290 295
110 gtg gct gag atg tat gtt cat gga tgg gat tat cct ttg cat ttg gga 1086
111 Val Ala Glu Met Tyr Val His Gly Trp Asp Tyr Pro Leu His Leu Gly
112 300 305 310
114 gtt act gag gca gga gaa ggc gaa gat gga cgg atg aaa tct gcg att 1134
115 Val Thr Glu Ala Gly Glu Gly Glu Asp Gly Arg Met Lys Ser Ala Ile
116 315 320 325
118 gga att ggg acg ctt ctt cag gac ggg ctc ggt gac aca ata aga gtt 1182
119 Gly Ile Gly Thr Leu Leu Gln Asp Gly Leu Gly Asp Thr Ile Arg Val
120 330 335 340
122 tca ctg acg gag cca cca gaa gag gag ata gat ccc tgc agg cga ttg 1230
123 Ser Leu Thr Glu Pro Pro Glu Glu Glu Ile Asp Pro Cys Arg Arg Leu
124 345 350 355
126 gct aac ctc ggg aca aaa gct gcc aaa ctt caa caa ggc gca ccg ttt 1278
127 Ala Asn Leu Gly Thr Lys Ala Ala Lys Leu Gln Gln Gly Ala Pro Phe

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131	Glu	Glu	Lys	His	Arg	His	Tyr	Phe	Asp	Phe	Gln	Arg	Arg	Thr	Gly	Asp			
132						380					385				390				
134	cta	cct	gta	caa	aaa	gag	gga	gaa	gag	gtt	gat	tac	aga	aat	gtc	ctt		1374	
135	Leu	Pro	Val	Gln	Lys	Glu	Gly	Glu	Glu	Val	Asp	Tyr	Arg	Asn	Val	Leu			
136					395				400					405					
138	cac	cgt	gat	ggt	tct	gtt	ctg	atg	tcg	att	tct	ctg	gat	caa	cta	aag		1422	
139	His	Arg	Asp	Gly	Ser	Val	Leu	Met	Ser	Ile	Ser	Leu	Asp	Gln	Leu	Lys			
140				410				415					420						
142	gca	cct	gaa	ctc	ctc	tac	aga	tca	ctc	gct	aca	aag	ctt	gtc	gtg	ggt		1470	
143	Ala	Pro	Glu	Leu	Leu	Tyr	Arg	Ser	Leu	Ala	Thr	Lys	Leu	Val	Val	Gly			
144		425					430					435							
146	atg	cca	ttc	aag	gat	ctg	gca	act	gtt	gat	tca	atc	tta	tta	aga	gag		1518	
147	Met	Pro	Phe	Lys	Asp	Leu	Ala	Thr	Val	Asp	Ser	Ile	Leu	Leu	Arg	Glu			
148	440					445				450				455					
150	cta	ccg	cct	gta	gat	gat	caa	gtg	gct	cgt	ttg	gct	cta	aaa	cgg	ttg		1566	
151	Leu	Pro	Pro	Val	Asp	Asp	Gln	Val	Ala	Arg	Leu	Ala	Leu	Lys	Arg	Leu			
152					460				465					470					
154	att	gat	gtc	agt	atg	gga	gtt	ata	gca	cct	tta	tca	gag	caa	cta	aca		1614	
155	Ile	Asp	Val	Ser	Met	Gly	Val	Ile	Ala	Pro	Leu	Ser	Glu	Gln	Leu	Thr			
156				475				480					485						
158	aag	cca	ttg	ccc	aat	gcc	atg	gtt	ctt	gtc	aac	ctc	aag	gaa	cta	tct		1662	
159	Lys	Pro	Leu	Pro	Asn	Ala	Met	Val	Leu	Val	Asn	Leu	Lys	Glu	Leu	Ser			
160		490					495					500							
162	ggt	ggc	gct	tac	aag	ctt	ctc	cct	gaa	ggt	aca	cgc	ttg	gtt	gtc	tct		1710	
163	Gly	Gly	Ala	Tyr	Lys	Leu	Leu	Pro	Glu	Gly	Thr	Arg	Leu	Val	Val	Ser			
164		505					510				515								
166	cta	cga	ggc	gat	gag	cct	tac	gag	gag	ctt	gaa	ata	ctc	aaa	aac	att		1758	
167	Leu	Arg	Gly	Asp	Glu	Pro	Tyr	Glu	Glu	Leu	Glu	Ile	Leu	Lys	Asn	Ile			
168	520					525				530				535					
170	gat	gct	act	atg	att	ctc	cat	gat	gta	cct	ttc	act	gaa	gac	aaa	gtt		1806	
171	Asp	Ala	Thr	Met	Ile	Leu	His	Asp	Val	Pro	Phe	Thr	Glu	Asp	Lys	Val			
172				540					545					550					
174	agc	aga	gta	cat	gca	gct	cgg	agg	cta	ttc	gag	ttc	tta	tcc	gag	aat		1854	
175	Ser	Arg	Val	His	Ala	Ala	Arg	Arg	Leu	Phe	Glu	Phe	Leu	Ser	Glu	Asn			
176				555				560					565						
178	tca	gtt	aac	ttt	cct	gtt	att	cat	cac	ata	aac	ttc	cca	acc	gga	atc		1902	
179	Ser	Val	Asn	Phe	Pro	Val	Ile	His	His	Ile	Asn	Phe	Pro	Thr	Gly	Ile			
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183	His	Arg	Asp	Glu	Leu	Val	Ile	His	Ala	Gly	Thr	Tyr	Ala	Gly	Gly	Leu			
184		585					590				595								
186	ctt	gtg	gat	gga	cta	ggt	gat	ggc	gta	atg	ctc	gaa	gca	cct	gac	caa		1998	
187	Leu	Val	Asp	Gly	Leu	Gly	Asp	Gly	Val	Met	Leu	Glu	Ala	Pro	Asp	Gln			
188	600					605				610				615					
190	gat	ttt	gat	ttt	ctt	agg	aat	act	tcc	ttc	aac	tta	tta	caa	gga	tgc		2046	
191	Asp	Phe	Asp	Phe	Leu	Arg	Asn	Thr	Ser	Phe	Asn	Leu	Leu	Gln	Gly	Cys			
192					620				625					630					

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199 Arg Thr Leu Phe Asp Leu Gln Glu Ile Ser Ala Glu Ile Arg Glu Lys
200          650          655          660
202 act tcc cat tta cct ggc gtt tgc atc gca atc atg gga tgc att gtg      2190
203 Thr Ser His Leu Pro Gly Val Ser Ile Ala Ile Met Gly Cys Ile Val
204          665          670          675
206 aat gga cca gga gaa atg gca gat gct gat ttc gga tat gta ggt ggt      2238
207 Asn Gly Pro Gly Glu Met Ala Asp Ala Asp Phe Gly Tyr Val Gly Gly
208 680          685          690          695
210 tct ccc gga aaa atc gac ctt tat gtc gga aag acg gtg gtg aag cgt      2286
211 Ser Pro Gly Lys Ile Asp Leu Tyr Val Gly Lys Thr Val Val Lys Arg
212          700          705          710
214 ggg ata gct atg acg gag gca aca gat gct ctg atc ggt ctg atc aaa      2334
215 Gly Ile Ala Met Thr Glu Ala Thr Asp Ala Leu Ile Gly Leu Ile Lys
216          715          720          725
218 gaa cat ggt cgt tgg gtc gac ccg ccc gtg gct gat gag tag      2376
219 Glu His Gly Arg Trp Val Asp Pro Pro Val Ala Asp Glu
220          730          735          740
222 atttcaaaac ggagaaagat ggggtgggcca ttctttgaaa actgtgagag aagatatata      2436
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234 <220> FEATURE:
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253 tcgcgtaggt ttccctacgg aagagctgag ttctgtaacg aaaaaaacgg gccacgtttc      180
255 gcatcgagcc tactttaatt agcgtgggaa aataattcaa agtagcgacc tgtaccctgt      240
257 ggcaacctag cgcgcgcggc catggtcttt gtccgctcgc tgacagtgtc cctgttcgcc      300
259 ggctcatgcc tcggatcagc gccgccgacg acatcgccgg cggcgtcggc ggcgtccacg      360
261 gcgacacgta cggtagtagt cgacggcatt acggccatct acaaacctcg gcgactcgct      420
263 gtcggacacc gcaacctcgc caggcaaggc gccaccggcg ggctgctccg gtacaccacg      480
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271 tggatatgat cgatcgatgt gcagctagag atcttggcct cctctgctc aaccgctacc 720
273 tcgacgagg cgcggaattc gccacggcg tcaacttcgc cgtcgccggc gccaccggcg 780
275 tcaacacgac ggcgctcgcc gccaggcgga tcaccgtccc ccacaccaac agccccctcg 840
277 acgtgcagct cagatttttt ttgttttaga gaagggtatt ttttaccggg cctctacatc 900
279 caaccggata tatacggcta ttgaagtagg gaacttaacc ctgtaaaaca tccatccata 960
281 gaggatatga acctaaagacc ttgaggtact acttcaaccg gatataacg tgcagctcag 1020
283 atggttcaag gaattcatga actccacaac tagttctcct caagggtgaa gaacaaactg 1080
285 aaacgcattt cagcttaatt tcgaccgggt cctgatcagt gccagtcagc aatgctgtat 1140
287 ctcaaaaata attaaagctaa tgtacagctt ttcagtgcga gaatgacttt catatagaga 1200
289 aatcttgtgt tatatatata tacttttttc tgaagaaaaa aagttctttt gtgtgagcat 1260
291 tgcattgcag agatccgtga aaagctgtcg aagtcactgg ttatgctggg agagatcgga 1320
293 ggaaacgact acaactacgc ctctctccag acctggccga tggacgggtg atacagcctc 1380
295 ggcaacgtca cacgcatgat cgaaagcggt gccacggcgg tcgatcttgt accggaagtc 1440
297 gtgcagcca tagccagcgc agccaaggta cacaccattc ttttccatta atttttggga 1500
299 ccttattttt aaaataataa tcttggttac aaagtaatta attaagaact aaattaattt 1560
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307 cgtggctgcg ccgcgcgcgt ggggagctgc ggcgcgcgta ccggggcgcc gcggtggtcg 1800
309 cgtacgcgga ctactccgcc gcgtacgcgc gcagcgtgga cggggcagcg gcgctgggct 1860
311 tcgacgagcg gcgcgtgttc agggcggtgt gcggcaaggg cggcgggggc gcgtacgggt 1920
313 tcgacgtgcg cgcgatgtgc ggcgcgcggg ggacggcggc gtgcgcggac ccggggaggt 1980
315 acgtgagctg ggacggcgtc cactgacgc agcgcgcgta cggcgctcat gccgagctgc 2040
317 tgttccgcgc tggcctcggt caccgcctc cgataaattt caccgaacgc gcgcgcgcgt 2100
319 gaggcgggtg tgcattgctt gcgcgttttt tctgatcaaa actactcaag tttgagccgt 2160
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361 tactttaaat gctttcaagt acaaagtgtt taaactacaa agtggttagat cccgttgagc 3420
363 tctacaactt tgatatggaa cacatctcca tcagatgtcg tttgaattgt agatctgaga 3480

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Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:821 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:1759 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:1763 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:1765 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:1767 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:1769 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:1798 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:1881 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:1883 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:1885 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:1887 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
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L:1948 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1950 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
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L:2064 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
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L:2219 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
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L:2836 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43
L:2840 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43